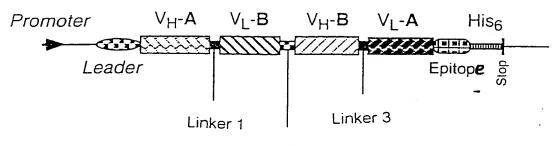
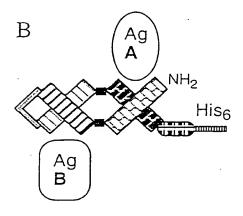
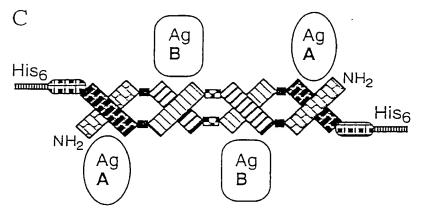
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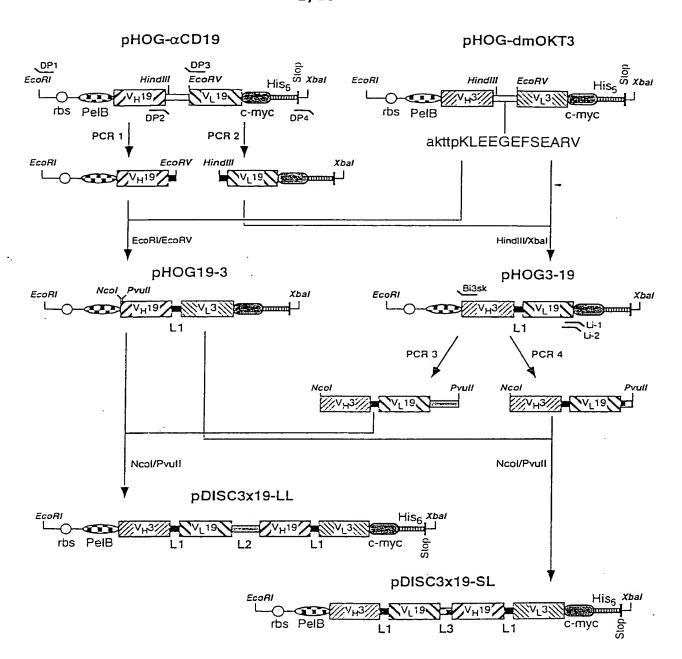


Linker 2





2/10



Linkers: L1 = GG

 $L2 = (G_4S)_4$

L3 = GGPGS

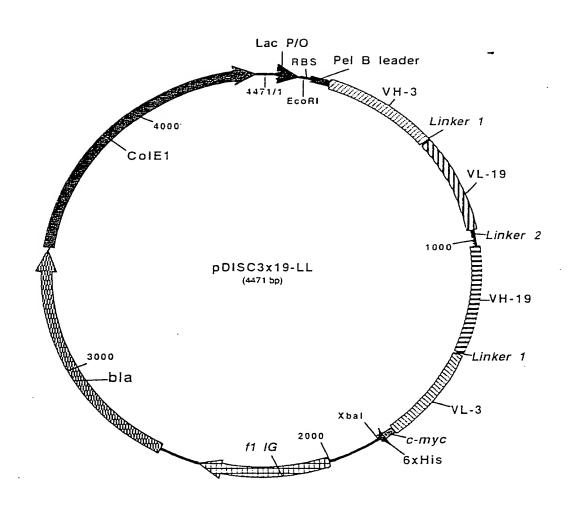


FIGURE 3

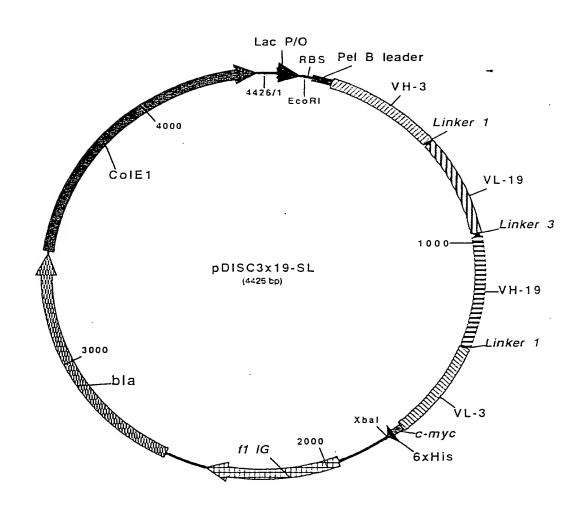


FIGURE 4

EcoRI ABS PelB leader Ncol
1 GAATTCATTAAAGAGAAGAAATTAACCATGAAATACCTATTSCCTTACGGCAGCCGCTGGCTGCTTGCTGCTGCCAGCCTCACCTGGCCAATGG
D M K Y L E P T A A A G L L L L A A Q P A M
Frame-H1 VH anti-C03
92 CGCAGGTGCAACTGCAGCAGTCTGGGGGTGAACTGGCAAGACCTGGGGGCCTCAGTGAAGATGTCCTGCAAGGCTTCTGGCTACACCTTTTAC
22 A Q V Q L Q Q S G A E L A R P G A S V K M S C K A S G Y T F T CDR-H1 Frame-H2 CDR-H2
183 TAGGTACACGATGCACTGGGTAAAACAGAGGCCTGGACAGGGTCTGGAATGGATTGGATTACATTAATCCTAGCCGTGGTTATAC
52 RYTMHWVXQRPGQGLEWIGYINPSRGYT Frame-H3
257 TAATTACAATCAGAAGTTCAAGGACAAGGCCACATTGACTACAAAATCCTCCAGCACAGCCTACATGCAACTGAGCAGCCAGC
30 N Y N Q K F K D K A T L T T D K S S S T A Y M Q L S S L T CDR-H3 Frame-H4
354 ATCTGAGGACTCTGCAGTCTATTACTGTGCAAGA <u>TATTATGATGATCATTACAGCCTTGACTAC</u> TGGGGCCCAAGGCACCACTCTCA
109 SEDSAVYYCARYYDDHYSLDYWGQGTTL
CH1 Linker 1 Frame-L1 VL anti-CD19
440 CAGTOTOCTCAGCCAAAACAACACCCCAAAGGTTGGGGGGTGATATGTTGCTCACCCAAACTCCAGCTTCTTTGGCTGTGTGTCTCTACGGCAGA
138 °T V S S A K T T P K L G G D I L L T Q T P A S L A V S L G Q COR-L1 Frame-L2
530 GGGCCACCATCTCCTGCAAGGCCAAAGTGTTGATTATGATGGTGATAGTTATTTGAACTGGTACCAACAGATTCCAGGAC
158) RATISCKASQSVDYDGDSYLNWYQQIPG
CDR-L2 Frame-L3
614 AGCCACCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGATCCCACCCA
CDR-L3 Frame-L4
702 CACCOTTCAACATCCATCCATCACACAACATCCTATCACATATCACATATCACATACTCATCA
225 T L N I H P 7 E K V D A A T Y H C Q Q S T E D P W T F G G
Ckacca Notl Linker 2
790 GGCACCAAGCTGGAAATCAAA <u>CGGGGTGATGCT</u> GCGGCGGCTGGTGGTGGTGGTTGTGGCGGGGGTGGTAGCGGTGGTGGCGGC
255 G T K L E I K R A D A A A A G G G G G G G G G G G
Pvull Frame-H1 VH anti-CD19
Pvull Frame-H1 VH anti-CD19 874 <i>TCCGGTGGTGGTGGTAGC</i> CAGCTGCAGCAGTCTGGGCTGAGCTGA
Pvull Frame-H1 VH anti-CD19 874 TCCGGTGGTGGTAGCCAGCTGCAGCTGCAGCAGTCTGCGGCCTGAGCCTGAGGCCTGGGTCCTCAGTGAAGATTTCCTGCAAGG 283 S G G G S Q V Q L Q Q S G A E L V R P G S S V K I S C K
Pvull Frame-H1 VH anti-CD19 874 TCCGGTGGTGGTAGCCAGCTGCAGCTGCAGCAGTCTGGGGCTGAGCTGGGTCCTCAGTGAAGATTTCCTGCAAGG 283 S G G G S Q V Q L Q Q S G A E L V R P G S S V K I S C K CDR-H1 Frame-H2 CDR-H2
Pvull Frame-H1 VH anti-CD19 874 TCCGGTGGTGGTAGCCAGCTGCAGCTGCAGCAGTCTGCGGCCTGAGCCTGAGCCTGAGCCTGAGCAGTCTCAGTGAAGATTTCCTGCAAGG 283 S G G G S Q V Q L Q Q S G A E L V R P G S S V K I S C K
Pvull Frame-H1 VH anti-CD19 874 TCCGGTGGTGGTAGCCAGGTCCAGCTGCAGCAGTCTGGGGCTGAGCTGAGGCCTGAGGCCTGAGGAGATTTCCTGCAAGG 283 S G G G S Q V Q L Q Q S G A E L V R P G S S V K I S C K CDR-H1 Frame-H2 CDR-H2 962 CTTCTGGCTATGCATTCAGTAGCTAGGATGAACTGGGTGAAGCAGGGCCTTGACAGGGTCTTGAGTGGATTGGACAGATTTGGC
PVUII Frame-H1 VH anti-CD19 874 TCCGGTGGTGGTAGCCAGTCCAGCTGCAGCAGTCTGGGCCTGAGCTGAGCCTGGGCCTGAGCTCAGTGAAGATTTCCTGCAAGG 283 S G G G S Q V Q L Q Q S G A E L V R P G S S V K I S C K CDR-H1 Frame-H2 CDR-H2 962 CTTCTGGCTATGCATTCAGTAGCTAGTGGATGAACTGGGTGAAGCAGGGCCTTGGACAGGGTCTTGAGTGGATTGGACAGATTTGGC 312 A S G Y A F S S Y W M N W V K Q R P G Q G L E W I G Q I W PStI Frame-H3 1049 CTGGAGATGGTGATGCAATGCAATGGAAAGTTCAAGGGTAAAGCCACTCTGACTGCAGACGAATCCTCCAGCACAGCCTACA
PVUII Frame-H1 VH anti-CD19 874 TCCGGTGGTGGTAGCCAGGTCCAGCTGCAGCAGTCTGGGGCTGAGCTGAGGCCTGGGTCCTCAGTGAAGATTTCCTGCAAGG 283 S G G G S Q V Q L Q Q S G A E L V R P G S S V K I S C K CDR-H1 Frame-H2 CDR-H2 962 CTTCTGGCTATGCATTCAGTAGCTAGGATGAACTGGGTGAAGCAGGGCCTTGACAGGGTCTTGAGTGGATTGGACAGATTTGGC 312 A S G Y A F S S Y W M N W V K Q R P G Q G L E W I G Q I W PStI Frame-H3
PVUII Frame-H1 VH anti-CD19 874 TCCGGTGGTGGTGGTGCAGCTGCAGCTGCAGCAGCTGCAGCTGAGGCTGAGGCCTGAGGCCTGAGGAGATTTCCTGCAAGG 283 S G G G S Q V Q L Q Q S G A E L V R P G S S V X I S C X CDR-H1 Frame-H2 CDR-H2 962 CTTCTGCCTATGCATTCAGTAGCTGGATGGAACTGGGTGAAGCAGGGCCTGGACAGGGTCTTGAGTGGATTGGACAGAGTTTGGC 312 A S G Y A F S S Y W M N W V X Q R P G Q G L E W I G Q I W PStI Frame-H3 1049 CTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAGGGTAAAGCCACTCTGACTGCAGACGAATCCTCCAGCACAGCCTACA 341 P G D G D T N Y N G X F X G X A T L T A D E S S S T A Y
PVuII Frame-H1 VH anti-CD19 874 TCCGGTGGTGGTGGTGGTCCAGTGCAGCTGCAGCAGCTGCAGCAGCTGAGCCTGAGGCCTGAGGCCTGAGGCTGAGAGATTTCCTGCAAGG 283 S G G G G S Q V Q L Q Q S G A E L V R P G S S V X I S C X CDR-H1 Frame-H2 CDR-H2 962 CTTCTGCCTATGCATTCAGTAGCTACTGGATGAACTGGGTGAAGCACAGGCCTGACAGGGTCTTGAGTGGATGGA
PVuII Frame-H1 VH anti-CD19 874 TCCGGTGGTGGTGGTGGTCCAGCTGCAGCAGCTGCAGCAGCTGAGCCTGAGCCTGAGCCTGAGCCTGAGCAGATTTCCTGCAAGG 283) S G G G G S Q V Q L Q Q S G A E L V R P G S S V X I S C X CDR-H1 Frame-H2 CDR-H2 962 CTTCTGGCTATGCATTCAGTAGCTACTGGATGAACTGGGTGAACCAGCCTGGACAGAGGTCTTGAGTGGACAGAGTTTGGCC 312) A S G Y A F S S Y W M N W V X Q R P G Q G L E W I G Q I W PStI Frame-H3 1049 CTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAGGGTAAAGCCACTCTGACTGCACGACGAATCCTCCAGCCCTACA 341) P G D G D T N Y N G X F X G X A T L T A D E S S S T A Y CDR-H3 1133 TGCAACTCAGCAGCCTAGCATCTGAGGACCTCTGCGGTCTATTTCTGTGCAAGAGGGGGGGG
PVuII Frame-H1 VH anti-CD19 874 TCCGGTGGTGGTGGTAGCCAGCTCCAGCTGCAGCAGCTGGGCCTGAGCCTGAGGCCTGGGCCTCAGTGAAGATTTCCTGCAAGG 283) S G G G G S Q V Q L Q Q S G A E L V R P G S S V X I S C X CDR-H1 Frame-H2 CDR-H2 962 CTTCTGGCTATGCATTCAGTAGCTACTGGATGAACTGGGTGAAGCAGAGCCTGGACAGGGTCTTGAGTGGACAGAGTTTGGACAGATTTGGC 312) A S G Y A F S S Y W M N W V X Q R P G Q G L E W I G Q I W PStI Frame-H3 1049 CTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAGGGTAAAGCCACTCTGACTGCAGAGAATCCTCCAGCACAGCCTACA 341) P G D G D T N Y N G X F X G X A T L T A D E S S S T A Y CDR-H3 1133 TGCAACTCAGCAGCCTAGCATCTGAGGACTCTGCGGTCTATTTCTGTGCAAGACGGGGAGACTACGACGGTAGGCCGTTATTACTAT 369) M Q L S S L A S E D S A V Y F C A R R E T T T V G R Y Y Y Frame-H4 CH1 Linker 1 Frame-L1 1219 GCTATGGACTACTGGGGTCAAGGACCTCAGCCTACCTCCAGCCAAGCTTGGCGGTGATATCGTGCTCACTC
PVuII Frame-H1 VH anti-CD19 874 TCCGGTGGTGGTGGTGGTGCAGCTCCAGCTGCAGCAGCTGGGCCTGAGCTGGGCCTGAGCTGGGCCTGAGCAGATTTCCTGCAAGG 283) S G G G G S Q V Q L Q Q S G A E L V R P G S S V X I S C X CDR-H1 Frame-H2 CDR-H2 962 CTTCTGGCTATGCATTCAGTAGCTACTGGATGAACTGGGTGAAGCACAGGCCTGGACAGGGTCTTGAGTGGACAGAGTTTGGACAGATTTGGC 312) A S G Y A F S S Y W M N W V X Q R P G Q G L E W I G Q I W PStI Frame-H3 1049 CTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAGGGTAAAGCCACTCTGAACTACTGCAGAATCCTCCAGCACAGCCTACA 341) P G D G D T N Y N G X F X G X A T L T A D E S S S T A Y CDR-H3 1133 TGCAACTCAGCAGCCTAGCATCTGAGGACTCTGCGGTCTATTTCTGTGCAAGACGGGGAGACTACGACGGTAGGCCGTTATTACTAT 369) M Q L S S L A S E D S A V Y F C A R R E T T T V G R Y Y Y Frame-H4 CH1 Linker 1 Frame-L1 1219 GCTATGGACTACTGGGGTCAAGGACCTCAGTCACCGTCTCACCTCCAGCCAAACCTTGGCGGTGATATCGTGCTCACTC 398) A M D Y W G Q G T S V T V S S A X T T P X L G G D I V L T
PVuII Frame-H1 VH anti-CD19 874 TCCGGTGGTGGTGGTGGTCAGTCAGTCAGCTGCAGCAGTCTGGGCTGAGCTGGGCCTGGGCCTCAGTGAAGATTTCCTGCAAGG 283 S G G G G S Q V Q L Q Q S G A E L V R P G S S V X I S C X CDR-H1 Frame-H2 CDR-H2 962 CTTCTGGCTATGCATTCAGTAGCTAGGTAGAACTGGGTGAAGCAGAGGCCTGGACAGGGTCTTCAGTGGATTGGACAGAGTTTGGC 312 A S G Y A F S S Y W M N W V X Q R P G Q G L E W I G Q I W PStI Frame-H3 1049 CTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAGGGTAAAGCCACTCTGACTGCAGACGAATCCTCCAGCACAGCCTACA 341 P G D G D T N Y N G X F X G X A T L T A D E S S S T A Y CDR-H3 1133 TGCAACTCAGCAGCCTAGCATCTGAGGACTCTTGGCAGAGGGTAAGCGGGTAAGCAGCTTATTTCTGTGCAAGACGGGGAGACTACGAGGGTGATATCATAT 369 M Q L S S L A S E D S A V Y F C A R R E T T T V V G R Y Y Y Frame-H4 CH1 Linker 1 Frame-L1 1219 GCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGAAACCTAGGGGTGATATCGTGCTCACTC 398 A M D Y W G Q G T S V T V S S A X T T P X L G G D I V L T VL anti-CD3 CDR-L1
PVUII Frame-H1 VH anti-CD19 874 TCCGGTGGTGGTGGTAGCCAGGTGCAGCAGCTGCAGCAGCTGCAGCGTGAGCGTGCTCAGGGGTCCTCAGTGAAGATTTCCTGCAAGG 283 S G G G G S Q V Q L Q Q S G A E L V R P G S S V X I S C X CDR-H1 Frame-H2 CDR-H2 962 CTTCTGCCTATGCATTCAGTAGCTACTGGATGAGTGGGTCAAGCAGAGGCCTTGACAGGGTCTTGAGTGGATTTGGC 312 A S G Y A F S S Y W M N W V X Q R P G Q G L E W I G Q I W PStI Frame-H3 1049 CTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAGGGTAAAGCCACTCTGACTGCAGACGAATCCTCCAGCACAGCCTACA 341 P G D G D T N Y N G X F X G X A T L T A D E S S S T A Y CDR-H3 1133 TGCAACTCAGCAGCCTAGCATCTGAGGACTCTGGGGTCTATTTCTGTGCAAGACGGAGACTACGAGGGTAGGCCGTTATTACTAT 369 M Q L S S L A S E D S A V Y F C A R R E T T T V G R Y Y Y Frame-H4 CH1 Linker 1 Frame-L1 1219 GCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCACCCCAAGCTTGACCTGACTGA
PVuII Frame-H1 VH anti-CD19 874 TCCGGTGGTGGTGGCCAGGTGCAGCTGCAGCAGCTGGGCGGTGAGCTGGTGAGCCTGGGGCCTGGTGCAGAGATTTCCTGCAGG 283 S G G G G S Q V Q L Q Q S G A E L V R P G S S V X I S C X CDR-H1 Frame-H2 CDR-H2 962 CTTCTGGCTATGCATTCAGTAGCTACTGGATGAACCTGGAGAGCAGAGGCCTGACAGGGTCTTGAGTGGATTGGACAGATTTGGC 312 A S G Y A F S S Y W M N W V X Q R P G Q G L E W I G Q I W PStI Frame-H3 1049 CTGGAGATGGTGATACTACATAGAATGGAAAGTTCAAAGGGTAAAGCCACTCTGACTGCAGACGAATCCTCCAGCACAGCCTACA 341 P G D G D T N Y N G X F X G X A T L T A D E S S S T A Y CDR-H3 1133 TGCAACTCAGCAGCCTAGCATCTGAGGACTTCTGGGTGAAGGCGGGGAGACTACGAGGGGGAGGCGGTAATTACTAT 369 M Q L S S L A S E D S A V Y F C A R R E T T T V G R Y Y Y Frame-H4 CHI Linker 1 Frame-L1 1319 GCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGAACCAACC
PVuII Frame-H1 VH anti-CD19 874 TCCGGTGGTGGTGGCCAGTGCAGCTGCAGCAGCAGCTGGGCTGAGCTGGTCCTCAGTGAAGATTTCCTGCAAGG 283) S G G G G S Q V Q L Q Q S G A E L V R P G S S V X I S C X CDR-H1 Frame-H2 962 CTTCTGCCTATGCATTCAGTAGCTACTGGATGGACTGGACTGGACAGGGCTTGACAGGGCTTGACAGGGCTTGACAGAGTTTGACAGAATTTGGCCAGAGTTTGACAGAACTGGATTTGACAGAACTGGACTGGACAGGGCTTGACAGGGCTTGACAGGGCTTGACAGAGTTTGACAGAATTCAGACGAATTCAGACGAATTCAGACAAATTCAGACAGA
PVuII Frame-H1 VH anti-CD19 874 TCCGGTGGTGGTGGTGGCAGCTGCAGCAGCTGCAGCAGCTGGGCGGGTGAGGCTGGGTCCTCAGTGAAGATTTCCTGCAAGG 283) S G G G G S Q V Q L Q Q S G A E L V R P G S S V X I S C X CDR-H1 Frame-H2 CDR-H2 962 CTTCTGCCTATCCATTCAGTAGCTACTGGATGAACTGGGTGAAGCAGGCCTGGACAGGGCTTTGAGTGGATTGGACAGGATTTGGC 312) A S G Y A F S S Y W M N W V X Q R P G Q G L E W I G Q I W PSII Frame-H3 1049 CTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAGGGTAAAGCCACTCTGACTGCACAGGATCCTCAGCACAGCCTACA 341) P G D G D T N Y N G X F X G X A T L T A D E S S S T A Y CDR-H3 1133 TGCAACTCAGCAGCCTAGCATCTGAGGACTCTGCGGTCTATTTCTGTGCAAGAGGGGGGGG
PVuII Frame-H1 VH anti-CD19 874 TCCGGTGGTGGTGGCCAGTGCAGCTGCAGCAGCAGCTGGGCTGAGCTGGTCCTCAGTGAAGATTTCCTGCAAGG 283) S G G G G S Q V Q L Q Q S G A E L V R P G S S V X I S C X CDR-H1 Frame-H2 962 CTTCTGCCTATGCATTCAGTAGCTACTGGATGGACTGGACTGGACAGGGCTTGACAGGGCTTGACAGGGCTTGACAGAGTTTGACAGAATTTGGCCAGAGTTTGACAGAACTGGATTTGACAGAACTGGACTGGACAGGGCTTGACAGGGCTTGACAGGGCTTGACAGAGTTTGACAGAATTCAGACGAATTCAGACGAATTCAGACAAATTCAGACAGA
PVUII Frame-H1 VH anti-CD19 874 TCCGGTGGTGGTGGTGGCAGTGCAGCTGGCAGTGGGCAGTGGGCAGTGGGCGGGGCGGGGCGGGGAGAGATTGCGGAGGGCGGGGAGGCGGGGGGGG
PVUII Frame-H1 VH anti-CD19 874 TCCGGTGGTGGTGGTGGCCAGGTCCAGCAGGTCTGAGCAGTCTGAGCCTGGGTCCTCAGGAGAGTTTCCTGCAGG 283) S G G G G S Q V Q L Q Q S G A E L V R P G S S V K I S C K CDR-H1 Frame-H2 CDR-H2 962 CTTCTGCCTATGCATTCAGTAGCTACTGGATGAACTGGGTGAACCAGGGTCTTGAGTGGATTGGACAGGATTTGGC 312) A S G Y A F S S Y W M N W V X Q R P G Q G L E W I G Q I W PStI Frame-H3 1049 CTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAGGGTAAAGCCACTCTGACTGA
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PVUIL Frame-H1 VH anti-CD19 874 TCCGGTGGTGGTGGTGGCGGTGAGCAGTGCAGCAGCTGGAGCCTGGGCCTGGGTCCTCAGGAAGATTTCCTCAAGG 283) S G G G G S Q V Q L Q Q S G A E L V R P G S S V X I S C X CDR-H1 Frame-H2 CDR-H2 962 CTTCTGGCTATCCATTCACTAGCTACTGGAGTGAGCAGGCCTGAAGCAGGCCTTGACAGGTTTGAGTGGATTGAGCAGATTTGGC 312) A S G Y A F S S Y W M N W V X Q R P G Q L W I G Q I W PStI Frame-H3 1049 CTGGAGATGGTGATACTAACTACTATGGAAAGTTCAAGGGTAAAGCCACTCTGACTGCAGAGCAAATCCTCCAGCCTACA 241) P G D G D T N Y N G X F X G X A T L T A D E S S S T A Y CDR-H3 1133 TCCAACTCAGCAGCCTAGCATCTGAGGACCTCTGCGTCTATTTCTGTGCAAGACGGGAGCTAAGCGGTAAGGCGTTATTACTAT 369) M Q L S S L A S E D S A V Y F C A R R E T T T V V G R Y Y Y Frame-H4 CH Linker 1 Frame-L1 1219 GCTATGGACTACTGGGGTCAAGCACCTCAGCTCCTCCAGCCAAACCAAGCTTGGGGGAGATTTGGGGGTGATATCTGTCCACTC 398) A M D Y W G Q G T S V T V S S A X T T P X L G G D I V L T VL anti-CD3 CDR-H3 1307 AGTCTCCAGCAATCTGCGGTCAACCTCAGCTCACCCAAGCTCCAAGCTCAAGCTCCAAG
PvuII
PVUIL Frame-H1 VH anti-CD19 874 TCCGGTGGTGGTGGTGGAGCAGTGCAGCAGTGTGAGCAGTGTGGGCTGGGTCCTCAGGAAGATTTCCTCAAGG 283) S G G G G S Q V Q L Q Q S G A E L V R P G S S V X I S C X CDR-H1 Frame-H2 CDR-H2 962 CTTCTGGCTATGCATTCAGTAGCTAGTGGAGTGAGGCAGGC

EcoRI RBS PelB leader Ncol
1 GAATTCATTAAAGACCAGAAATTAACCATGAAATTACCATATTCCTATCCCTACCCCCACCCCCCCC
PMXYLLPTAAAGLLLAAQ.PAM
◆ Frame-H1 VH anti-CD3
92 CGCAGGTGCAACTGCAGCAGTCTGGGGGCTGAACTGGCAAGACCTGGGGGCCTCAGTGAAGATGTCCTGCAAGGCTTACTGGCTACACCTTTTAC
22 A Q V Q L Q Q S G A E L A R P G A S V K M S C K A S G Y T F T
CDR-H1 Frame-H2 CDR-H2 →
183 TAGGTACACGATGCACTGGGTAAAACAGAGGCCTGGACAGGGTCTGGAATGGATTAGATAAATCCTAGCCGTGGTTATAC
52) RYTMHWVXQRPGQGLEWIGYINPSRGYT
Frame-H3
267 TAATTACAATCAGAAGTTCAAGGACAAGGCCACATTGACTACAGACAAATCCTCCAGCACAGCACAGCATGCAACTGAGCAGCCTGAC
80 NYNQKFKDKATLTTDKSSSTAYMQLSSLT
CDR-H3 Frame-H4
354 ATCTGAGGACTCTGCAGTCTATTACTGTGCAAGA <u>TATTATGATGATCATTACAGCCTTGACTAC</u> TGGGGCCAAGGCACCACTCTCA
109 SEDSAVYYC'ARYYDDHYSLDYWGQGTTL
CH1 Linker 1 Frame-L1 VL anti-CD19
440 CAGTOTOCTCAGCCAAAACACCACCCAAGCTTGGCGGTGATATCTTGCTCACCCAAACTCCAGCTTCTTTGGCTGTGTGTCTTAGGGCAGA
138 T V S S A K T T F K L G G D I L L T Q T P A S L A V S L G Q
CDR-L1 Frame-L2
530 GGGCCACCATCTCCTGCAAGGCCAAGCCAAAGTGTTGATTATGATGGTGATAGTTATTTGAACTGGTACCAACACATTCCAGGAC
168 PRATISCKASQSVDYDGDSYLMWYQQIFG
COR-L2 Frame-L3 614 AGCCACCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGATCCCACCCA
196 Q P P K L L I Y D A S N L V S G I P P R F S G S G S G T D F
CDR-L3 : Frame-L4
FORMER: CHOOS CALCADE A TOTAL A CALCADA CONTRATO CALCADA CONTRATO CALCADA CONTRATO CONTRATA CONTRATO C
225° TLNIH PVEKVDAATYHCQQSTEDPWTFGG
Ckappa Notl Linker 3 Pyull Frame-H1
790 GGCACCAAGCTGGAAATCAAA <u>CGCCTGATGCT</u> GCGGCCGCTGGTGGGCCCAGGGTCGCAGGTGCAGCTGCAGCAGTCTGGGGCTGAGCT
255 G T K L E I K R A D A A A G G P G S Q V Q L Q Q S G A E L
VH anti-CD19 CDR-H1 Frame-H2
879 GGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTGCLAGGCTTCTGGCTATGCATTCAGT <u>A GCT A CT GGA TGA A C</u> TGGGTGAAGCAGAGGC
284 V R P G S S V K I S C K A S G Y A F S S Y W M N W V K Q R
CDR-H2
968 CTGGACAGGGTCTTGAGTGGATTGGATTTGGGCCTGGAGATGGTGATACTAACTA
968 CTGGACAGGGTCTTGAGTGGATTTGGAGATTTGGCCTGGAGATGGTGATACTAACTA
968 CTGGACAGGGTCTTGAGTGGACTGGAGATTTGGCCTGGAGATGGTGATACTAACTA
968 CTGGACAGGGTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGGTGATACTAACTA
968 CTGGACAGGGTCTTGACTGGACTGGACAGATTTGGCCTGGAGATGGTGATACTAACTA
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968 CTGGACAGGGTCTTGAGTGGATTTGACAGGTTATTGGCCTGGAGATGGTGATACTAACTA
968 CTGGACAGGGTCTTGAGTGGATTTGGCCTGGAGATTGGCTTGAGATTGAACTAACT
968 CTGGACAGGTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGGTGATACTACTACAATGGAAAGTTCAAGGGTAAAGCC 314) P G Q G L E W I G Q I W P G D G D T N Y N G K F K G K A Frame-H3 1051 ACTCTGACTGCAGGACGAATCCTCCAGCACACACTGCAACTCAGCACCCTAGCATCTGAGGACTCTCGGGTCTATTTCTGTGCAAGAC 342) T L T A D E S S S T A Y M Q L S S L A S E D S A V Y F C A R COR-H3 1142 GGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGACTCAGGGACCTCAGGACCTCAGGACCTCAGGCTCCTCAGCAACTCAGCACCTCAGCACCTCAGGACCTCAGGCACCTCAGGCAACCTCAGGCCGTCTCTCAGCCAAAA 372) R E T T T V G R Y Y Y A M D Y W G Q G T S V T V S S A K Linker 1 Frame-L1 VL anti-CD3 1226 CAACACCCAAACCTTGGCGGTGATATCGTGCTCACCAATCATGCTCCACCAATCATGCTCCAGGGGAGAAGGTCACCATGACCTGCA 400) T T P K L G G D I V L T Q S P A I M S A S P G E K V T M T C COR-L1 Frame-L2 1316 GTGCCAGCTCAAGTTGAGGTAACTTACATGAACTGCTCACCAAAAGATGGATTTATGACAACCATCCAA 430) S A S S S V S Y M N W Y Q Q K S G T S P K R W I Y D T S K Frame-L3 1401 ACTGGCTTCTGGAGTCCATCACCTTCAGGGCAACCTCCCCCAAAAAGATGGATTTATGACAACATCCAACCAA

98 GAELARPGASVKMSCKAS

941 ATGAGATTTCCTTCAATTTTTACTGCTGTTTTTATTCGCAGCATCCTCCGCATTAGCTGCTCCAGTCAACACTAC

1) M R F P S I F T A V L F A A S S A L A A P V N T T

alpha-factor signal

1015 AACAGAAGATGAAACGGCACAAATTCCGGCTGAAGCTGCATCATCGGTTACTCAGATTTAGAAGGGGATTTCGATG

25) T E D E T A Q I P A E A V I G Y S D L E G D F D

B\$rDI

1089 TTGCTGTTTTGCCATTTTCCAACAGCACAAATAACGGGTTATTGTTTATAAATACTACTATTGCCAGCATTGCT

50) V A V L P F S N S T N N G L L F I N T T I A S I A

EcoRI

XhoI

**EcoRI

1163 GCTAAAGAAGAAGAGGGGTATCTCTCGAGAAAAGAGAGGGCTGAAGCTGAATTCATGGCGCAGGTGCAACTGCAG

75) A K E E G V S L E K R E A E A E F M A Q V Q L Q

VH anti-CD3

1235 CAGTCTGGGGGCTGAACTGGCAAGACCTGGAGGTGCAAGGTTCT

S C K

99 Q S G A E L A R P G A S V K M

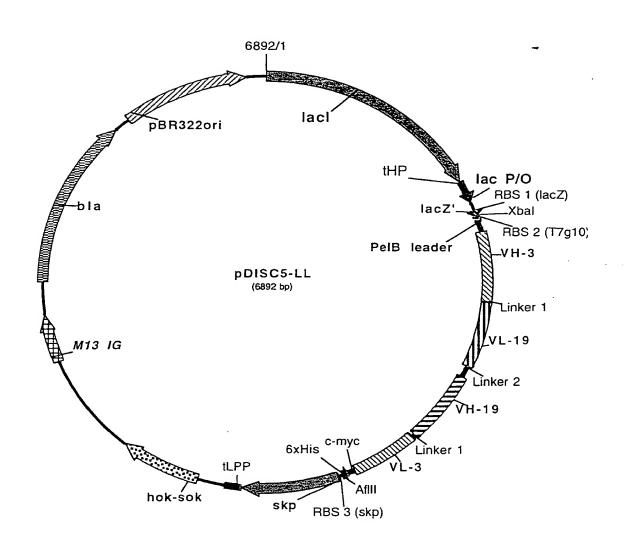


FIGURE 9

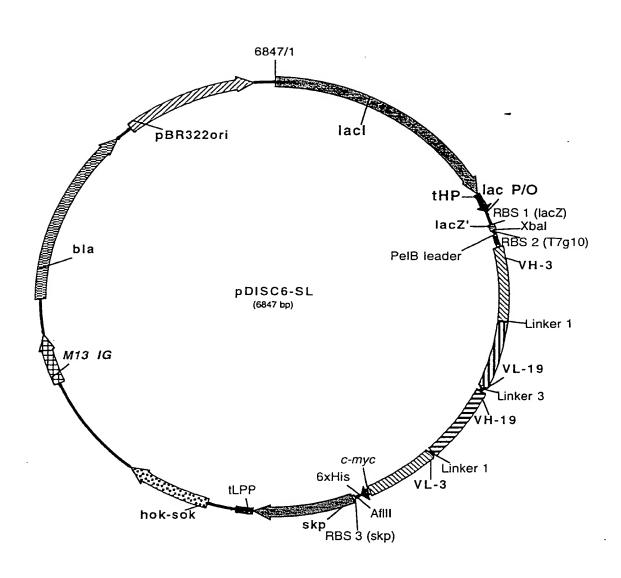


FIGURE 10